

GenCore version 4.5
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February 5, 2002, 16:26:13 : Search time 3596.51 Seconds
(without alignments)
2456.000 Million cell updates/sec

US-09-509-591-1

Direct score: 822
Sequence: 1 GCATTGCTGTGAACCTCTGTA.....TTCCACCACCTGCCAATAACA 822

Sorting table: IDENTITY_NUC
Capped 10 0

searched: 11351937 seqs, 5372889281 residues

total number of hits satisfying chosen parameters: 22703674

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num DB seq length: 0
xtlmm DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Listing first 45 summaries

```
Database : EST:*
```

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121: em_gss_fun: *
122: em_gss_hic: *
123: em_gss_inv: *
124: em_gss_pln: *
125: em_gss_pro: *
126: em_gss_rnd: *
127: em_gss_vrt: *
128: em_gss_othr: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Serial No.	Score	Query Match	Length	DB	ID
1	197.2	24.0	556	13	AQ0054022
2	85	10.3	873	10	A0121310
3	52.2	6.4	1101	13	CNS0100X
4	51.2	6.2	574	13	AQ03816
5	47	5.7	456	11	BF770244
6	46.4	5.6	553	13	AQ542774
7	46.2	5.6	749	13	AQ743295
8	45.4	5.5	534	13	BF770203
9	44.6	5.4	1101	13	CNS00393
10	44.2	5.4	551	13	AQ248008
11	43.8	5.3	364	10	AA587883
12	43.8	5.3	417	11	BF773318

Accession	Description
A00054.02	C14-HSP
A0121.910	A0121310
AL098379	Protophosph
A03861.65	HS_471212
BE77.0244	K3C-IT000
A0547.0774	PCP1-1111
A074339.9	HS_53877
BE77.0233	K3C-IT000
A01639.21	Dioproph1
A02480.96	HS_101514
AA5878.63	nm71a0514
BE77.73.18	CW1-IT000

C	13	43.8	5.3	450	10	A1392863
C	14	43.8	5.3	492	10	AM614814
C	15	43.8	5.3	360	13	B65091
C	16	42.6	5.2	487	13	AQ427571
C	17	42.6	5.2	587	13	B95393
C	18	42.4	5.2	347	13	AQ665278
C	19	42	5.1	797	13	CNS00368
C	20	42	5.1	1101	13	CNS002040
C	21	41.8	5.1	447	13	AQ204357
C	22	41.8	5.1	143	13	AQ314643
C	23	41.6	5.1	588	13	B46698
C	24	41.6	5.1	1101	13	CNS006238
C	25	41.2	5.0	537	11	BP003883
C	26	41.2	5.0	774	13	AQ375584
C	27	41.2	5.0	1101	13	CNS005EPA
C	28	41.2	5.0	1101	13	CNS005EPC
C	29	41.1	5.0	131	13	AQ104872
C	30	41.1	5.0	439	10	AA790739
C	31	41	5.0	1101	13	CNS01611
C	32	41	5.0	1201	13	CNS015E2
C	33	40.8	5.0	437	10	AAS32800
C	34	40.6	4.9	600	10	A1830342
C	35	40.4	4.9	584	13	AQ312805
C	36	40.4	4.9	928	13	CNS00DXY
C	37	40.4	4.9	1085	13	CNS00D7GH
C	38	40.4	4.9	1101	13	CNS017XX
C	39	40.2	4.9	544	13	AQ429595
C	40	40.2	4.9	548	10	BE030762
C	41	40.2	4.9	869	13	CNS00KRL
C	42	40	4.9	339	11	BE889090
C	43	40	4.9	876	13	AQ551355
C	44	40	4.9	856	13	AZ537553
C	45	40	4.9	920	13	AZ529784

ALIGNMENTS

[illegible]

RESULT	1
A0005402/c	
LOCUS	
DEFINITION	A0005402 556 bp DNA GSS 27-JUN-1998
DEFINITION	CIT:HSP-2293G2.TE CIT:HSP Homo sapiens genomic clone 2293G2, DNA sequence
ACCESSION	A0005402
VERSION	A0005402.1 GI:3082847
KEYWORDS	GSS,
SOURCE	human,
ORGANISM	Homo sapiens;
	Eukaryotes; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 556)

TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Mapping
JOURNAL	Building (1998)
COMMENT	Unpublished (1998)
CONTACT	CONTACT: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301.838.0200

Endeavour Publications
Endeavour Publications
Clones are available from Research Genetics (Inforesgen.com). BAC
end search page:
http://www.flygry/cdb/nungun/Bac_end_search/Bac_end_search.html
Send printer: ML3-21:

FEATURES	Location/Qualifiers
source	1 156
	/organism="Homo sapiens
	/db-ref="GDB:7151790"

BASE COUNT 168 a 55 c 130 g 103 t
 ORIGIN

Query Match 5.7%; Score 47; DB 11; Length 456;
 Best Local Similarity 58.0%; Pred. No. 1.8;
 Matches 83; Conservative 0; Mismatches 60; Indels 0; Gaps 0

2Y 182 ATGGTCACATTAACGTCTGCAAGCTTATGATCCCAATATATCTAGCCCTCAATC 211
 2Y 317 ATAGATTAATATCCATTTCTATGATCAATACCTTCAATCTCAATCCACCCCAATC 258
 2Y 242 TTCTTCAGAAAGTAAAGATATATTCATATGACATCACTCACTTGGAGGCT 301
 2Y 257 TTGTCTCTGAACACAGAACACATCAGAGAGCTTTTGGACATCTCCACTAGACCTTC 198
 302 TAAAGAGCTTCAACATCAACAC 324
 197 CACAGACATCTCAGATCCGAAC 175

RESULT 6
 LOCUS AO542774 553 bp DNA 16-JUL-1999
 DEFINITION RPCI-11-361L13.TV RPCI-11 Homo sapiens genomic clone RPCI-11-361L13
 ' DNA sequence.

ACCESSION AO542774
 VERSION AO542774.1 GI:4873230
 KEYWORDS GSS.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 553)
 Zhao S., Adams M.D., Nierman W., Malek J., de Jong R. and Venter

AUTHORS

J.C.

TITLE

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready

JOURNAL

Map Building
 Unpublished (1997)
 Contact: Shaying Zhao, William Nierman, Mark Adams

COMMENT

Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeef@igf.org

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.bufralo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.bufralo.edu/ordering>) or from
 Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.htm
 Seq primer: T7
 Class: BAC ends.

FEATURES

Location/Qualifiers

1..553
 /organism="Homo sapiens"
 /db_xref="GDB:7638516"
 /db_xref="taxon:9606"
 /clone="RPCI-11-361L13"
 /clone_id="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; site_1: EcoRI; site_2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT

169 a 121 c 84 g 179 t

Query Match 5.6%; Score 46.4; DB 13; Length 553;
 Best Local Similarity 62.9%; Pred. No. 2.4;
 Matches 88; Conservative 0; Mismatches 51; Indels 1; Gaps 1

OY 142 TTCTCTTCACTGCACTGCTAATA-TTTTTCACACCTCAGAGGTACATACCTCT 200
 DB 346 TTTCATGATGATCTGCTGCTGCTATCTCATTCAGCTTCAGCTTTAAATACCTCT 405
 OY 201 GCAAGTTATGATCCCAATATCTATCTAGCTCAATCTTGTCCAGAAATAAAT 260
 DB 406 CTATACATGATCTTCAATATATAGCTCAGCTGATGTGAATCCAGATGTACTAT 465
 OY 261 GATGATATCAATGCAATC 280
 DB 466 GTAGCTTCTACCTGGACATC 485

RESULT 7
 LOCUS AO743299 749 bp DNA 16-JUL-1999
 DEFINITION HS-5387.B2.A08.SP6.RPCI-11 Human Male BAC Library Homo sapiens
 genomic clone Plate-963 Col-16 Row-B, DNA sequence.
 ACCESSION AO743299 GI:5520821
 VERSION AO743299.1 GI:5520821
 KEYWORDS GSS.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 749)
 Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
 Kellner A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.

AUTHORS

Sequence tagged connectors: A sequence approach to mapping and
 scanning the human genome

TITLE

Sequence tagged connectors: A sequence approach to mapping and
 scanning the human genome

JOURNAL

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 99380589

MEDLINE

Contact: Mahairas G.G., Wallace J.C., Hood L.
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: j.wallace@u.washington.edu

COMMENT

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.bufralo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.bufralo.edu/ordering>) or from
 Research Genet cs (info@resgen.com). BAC end web Server:
<http://www.htsc.washington.edu>
 Plate: 963 Row: B column: 16
 Seq primer: SP6
 Class: BAC ends.

High quality sequence stop: 749.
 Location/Qualifiers

1..749
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-963 Col-16 Row-B"
 /clone_id="RPCI-11 Human Male BAC Library"
 /sex="Male"
 /note="Vector: pBAC3.6; site_1: EcoRI; site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI-Methyase. Site selected DNA was cloned into the
 pBAC3.6 Vector at EcoRI sites"

BASE COUNT

181 a 190 c 166 g 212 t

ORIGIN

Query Match 5.6%; Score 46.2; DB 13; Length 749;
 Best Local Similarity 58.3%; Pred. No. 2.5;
 Matches 81; Conservative 0; Mismatches 58; Indels 0; Gaps 0
 OY 111 CTGCTTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 170

b	363	CTGGCATGAGATTAATAAGATTCTTCACAGCCTTACAGCGGTGTCTTTTCAGAGTGCGCT	422
y	171	CAACCACTCACATGCGTAACTACTGTCTGCAGCTAATGAATCCCAATATCATCTC	230
b	423	CACACCTCCCATGCGCTCAGATACCTCTGCCGCTGGAGGATCTGCACATTATAGCCCTC	482
y	231	TACCCTCAATCTGTTCGA	249
b	483	CAGCTTAGATGCTTACGA	501

RESULT	8		
LOCUS	BF770233/c	534 bp	mRNA
DEFINITION	RC3-IT0022-201100-021-c07 IT0022 Homo sapiens CDNA, mRNA sequence	EST	12-JAN-2001
VERSION	BF770233		
KEYWORDS	BF770233.1 GI:12118133		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 534) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R. Nagel,M.A., de Saliva,W. Jr., Zagor,M.A., Bordin,S., Costa,F.F., Goldman,G.H., deOliveira,A.F., Matsushima,A., Bala,G.S., Simpson,D.H. Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare, M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496 (2000)
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genom Project. This entry can be seen in the following URL: (http://www.ludwig.org.br/scripts/gethtml2.pl?rl=NC3&c2=NC3-IT002 201100-021-c07&t3=2000-11-20&t4=1) Seq primer: puc 18 forward High quality sequence start: 50 High quality sequence stop: 444. Location/Qualifiers 1. 534 /organism="Homo sapiens" /db_xref="taxon:9606" /clone-lib="IT0022" /dev-stage="Adult" /note="Organ: epid.tumor; Vector: puc18; Site1: Smal; Site2: SmaI; A mini-library was made by cloning product derived from ORESTES PCR (U.S. Letters Patent applicati No. 196,716 - Ludwig Institute for Cancer Research). Profiles Info The puc 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions."		

BASE COUNT	191 a	83 c	148 g	112 t
ORIGIN				

Query Match	5.5%	Score 45.4;	DB 11;	Length 534
Best Local Similarity	57.3%;	Pred. No. 4;		
Matches 82;	Conservative 0;	Mismatches 61;	Indels 1;	Gaps 0

182	ATGCGTCATCAATCTGCTCAGACTTATATATCCCAATATATCTAGCGCTCAATC	241
b	11 GCTTTT 111111 111111 111111 111111 111111 111111 111111	
350	ATGATGCAATGCCATTTCATGCAATAGCCCTTCATATCTTATCTCAGCGCAATC	291

[illegible]

```

db 874 TNCASCTGTTGCTGCTGACATAATAATACAAATGACCGGTATGCTGTTATTTATGTCGAA 678
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db 934 HNNHNNMMMAATWTTTMTTMMSCSMNNHNNHMMHMMHMMSCCHUCSTCHNATTHNNM 993
y 679 ATGCGCCATTTTAAACCTAAAGAAATCCATTAAGTAAAGATTTACCAACAAAGGTTA 739
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db 1054 HMTTGTGCTGTTTMMHNNHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 1096

RESULT 10
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NITON HS-2015_A1_H03_MR_CIT Approved Human Genomic Sperm Library D homo
WCCSSION AQ248096 sapiens genomic clone Plate=2015 COL-5 Row=O, DNA sequence
VERSION AQ248096.1 GI:3698278
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo
1 (Passes 1 to 551)
Mahalax,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T. and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahalax GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu
Sequence Tagged Connector
Plate: 2015 row: 0 column: 5
Class: BAC ends
High quality sequence stop: 551.
location/Qualifiers
1. 551
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/db_xref="taxon:9606"
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E-col1 DH10B"
BASE COUNT 183 a 85 c 129 g 148 t 6 others
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Best Local Similarity 49.66; Pred. No. 7.3;
Matches 138; Conservative 0; Mismatches 139; Indels 1; Gaps 1;
y 46 CACACATAGATTTGAGATTTCTTCTGTATGACATACAAACTCTGGTTCAAGCTCCCTT 105
db 351 CACGGTTCCTTCAATTTCAAGTCTACTTACAAAGATTCCTCCCTTTCTTTACCTCAAAA 292
y 106 TATTCCTTCTTGGAATAATTTGCTGTTCTTCACTAGGTTTCTCTTTTCACTGTAATCTT 165
db 291 TTGAGATGATCCAAAGATCAATCTGTTGGTTCTTCTCCNTCTACAGCACTCCCTTGT 232
y 166 TTTCACACCACTCAATAGGTACAAATACAGTCTGCAAGCTTATGATTCACCAATTAATCT 225

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	DB	172	CATGTCACCTGAGTGTCAATGGCTTTAAATGCCTCTTAAGCTTGATGATCCATAATTAT	172
OY	226	ATCTCAGGCTCAATCTTGTCTCGAAGATATAAAGTAGTATTCAATGACATCACGT	285	
DB	171	ATTCGAGGCCAGATGTCTCTCTGACTCCACACC	113	
OY	286	CTCCACTGAGGCTTAAGAAGCTTCAACATACAA	323	
DB	112	ATTCCTTGATGATGCTAGCATCTCAATTATTA	75	
RESULT	11			
LOCUS	AA587883	364 bp	mRNA	EST
DEFINITION	hm714952 NC_1 CGAP_C03 Homo sapiens cDNA clone IMAGE:1073648	3'		
ACCESSION	AA587883			
VERSION	AA587883.1	G1.2402058		
KEYWORDS	EST			
SOURCE	human:			
ORGANISM	Homo sapiens:			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Euarchonta; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997).			
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-jrnell.nih.gov Issue Procurement: ilan.kirsch, M.D., Michael R. Emmert-Buck, M.D. Ph.D.			
COMMENT	cDNA library preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMW at: www.bio.liml.gov/dbip/image/image.html Seq primer: -40m3 fwd. Et from Amersham High quality sequence stop: 309.			
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BASE COUNT	68 a	132 c	60 g	104 t
ORIGIN				
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	Best Local Similarity	64.1%	Pred. No. 9.3;	
	Matches 66; Conservative 0;	Mismatches 37;	Indels 0;	Gaps 0;
OY	140	GGTTTCCTTTCACTGCTATATATTTTCTAACACCTGACATGGCTACATACTGC	199	
DB	19	GCTTCCAGAGATTCACCTTCCAGCTGTCTCATCCACCCATCCATGCTTCACTGCTACC	78	
OY	200	TGCAGCTTATGATCCCAAATATATATCTAGGCTCAACT	242	
DB	79	TCTGCGCACATGATTTTCAMATATGCCATGGCAGCTCCAACT	121	


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LOCUS       A1392863             450 bp     mRNA
DEFINITION  t905a08.x1 NC1-CEAP-CLL1 Homo sapiens CDNA clone IMAGE:2107862 3',
ACCESSION   A1392863
VERSION     A1392863.1
KEYWORDS    EST
SOURCE      human
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 450)
AUTHORS    NC1-CEAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL    Tumor Gene Index
COMMENT     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb1r@nci.nih.gov
Tissue/Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NC1-CEAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILWU at:
www.bio.ljll.gov/db/rrp/image/image.html
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High quality sequence stop: 433.
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/lab_host="DH10B"
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TGTATCCAAATCGAAGTGGGCGCGCCGACATGTTTATTTTATTTTATTTT
T 3.1; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pUT7 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonadio."
BASE COUNT      106 a 123 c 55 g 166 t
ORIGIN
106 a 123 c 55 g 166 t
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Best Local Similarity 56/68; Pred. No. 9.1;
Matches 81; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
CY 182 ATGGCTACAAATACGTCGCAAGTTATGATATCCCAATATATCTATCTGACCCATTC 241
DB 135 ATAGATTCAAAGCCATTTCATGATAGACCTTAATATCTCTATCTCCAGCCAAATC 194
CY 242 TTGTTCGAGAAATATAAAGTAGTATTCATAATGCACATCAACGTCCTGAGAGGCT 301
DB 195 TTGTTCGAGAACTCGAAGCCACATCTAGAGAAGTTTGTGACATCTCCACTGAGACGTC 254
CY 302 TTAAGCGTTTCAACATCAAC 324
DB 255 CACGACATCTCAGATCCGAAC 277
RESULT 14
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DEFINITION  hg50a02.x1 NC1-CEAP-Kid1 Homo sapiens cDNA clone IMAGE:2951882 3',
ACCESSION   A1614814

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ERSDON AM614814.1 GI:7320000
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo
 1 (bases 1 to 492)
 REFERENCE NC-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NC-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILM at:
 Image.llnl.gov/image/ilm/ILM/ILMResources.shtml
 Seq primer: -400p from GIBCO
 High quality sequence stop: 450.
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 plasmid DNA from the normalized library NC-CGAP_K1d3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clonoids 132376-132391, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldo."
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 140 GGTTCCTCTTTCACGCTATCTATTTCTCACCACACATCGCTACATTAATCTGTC 199
 |||||
 10 GGTTCACAGAGTTCATCTCCAGAGTCTCTCATCCATCCCATGCTCAGGCTACC 69;
 |||||
 200 TGCACCTTATGATTCCTCCAAATATCTATCTCTAGCCGCAATCT 242
 |||||
 70 TGGCGCAGATGATTTTCAATATCCCATGCGCAGCTCCCAATCT 112
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 LOCUS B65091 360 bp DNA GSS 21-JUN-1998
 DEFINITION CIT-HSP-201505.TRB CIT-HSP Homo sapiens genomic clone 201505 DNA
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 ACCESSION B65091
 VERSION B65091.1 GI:2639069
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo
 1 (bases 1 to 360)
 REFERENCE Adams,M.D., Rounsley,S.D., Field,C.E., Baas,S., Linher,K., Golden
 K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
 and Venter,J.C.

TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building
 JOURNAL Unpublished (1997)
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: madams@igf.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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 Location/Qualifiers
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 168 TCTCAACCACTCACAATGCTTACATATCTGCTGCAAGCTTATGATTCCTCAATATCTAT 227
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 199 TCTCATCTAGTCTGCAATGCTTAAATGCTTACTCTGATGATTCATATATATAT 140
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 228 CTCTACCTCAATCTGTTCTCAGAGATATAAAGTAGTATTCAAATGCACATCAAGTCT 287
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 139 CTCACCCAGATCTCTCTCCGAACTCCACACCCG-TATCAAGACCTTATGGCATAT 81
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 288 CCACTGGAGGCTTAAAGCTTCAATACAA 323
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 80 CCTTGAATGTTAGTACATCTCAAAATTTATA 45
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